WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Tuesday, June 20, 2006

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ		
☐	L4	L3 and mitoneet	4
☐	L3	L2 or l1	275
☐	L2	mcdonald near william	261
☐	L1	colca near jerry	17

END OF SEARCH HISTORY

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	10	colca near jerry	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/20 09:42
L2	241	mcdonald near william	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/20 09:42
L3	250	l1 or l2	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/20 09:42
L4	2	l3 and mitoneet	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/20 09:43
L5	4	mitoneet	US-PGPUB; USPAT; DERWENT	OR	ON	2006/06/20 09:43

```
=> d his

     (FILE 'HOME' ENTERED AT 09:47:05 ON 20 JUN 2006)

     FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:47:20 ON 20 JUN 2006
                E COLCA JERRY /AU
L1             90 S E3 OR E4
                E MCDONALD WILLIAM G /AU
L2             13 S E3
L3             96 S L1 OR L2
L4              5 S L3 AND MITONEET
L5              3 DUP REM L4 (2 DUPLICATES REMOVED)
L6              6 S MITONEET
L7              4 DUP REM L6 (2 DUPLICATES REMOVED)
```

=> d l7 1-4 ti au py so

L7 ANSWER 1 OF 4 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Receptor independent effects of thiazolidinediones in astrocytes.
AU Akar, C. A. [Reprint Author]; Colca, J.; Dello Russo, C.; Spagnolo, A.; Gavrilyuk, V.; Feinstein, D. L.
PY 2005
SO Journal of Neurochemistry, (JUN 2005) Vol. 94, No. Suppl. 1, pp. 41. Meeting Info.: 36th Annual Meeting of the American-Society-for-Neurochemistry. Madison, WI, USA. June 25 -29, 2005. Amer Soc Neurochem. CODEN: JONRA9. ISSN: 0022-3042.

L7 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN
TI Antisense modulation of **mitoneet** expression for treatment of diseases
IN Colca, Jerry R.
PY 2004
2005
2004
2004
2005
2005
2005
2006
2004
SO PCT Int. Appl., 226 pp.
CODEN: PIXXD2

L7 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2006 ACS on STN
TI Mitochondrial membrane **mitoNEET** proteins binding thiazolidindiones and their use in the development of novel antidiabetic agents
IN Colca, Jerry R.; McDonald, William G.
PY 2004
2005
2004
2004
2005
2005
2006
2005
SO PCT Int. Appl., 116 pp.
CODEN: PIXXD2

L7 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 1
TI Identification of a novel mitochondrial protein ("**mitoNEET**") cross-linked specifically by a thiazolidinedione photoprobe.
AU Colca Jerry R; McDonald William G; Waldon Daniel J; Leone Joseph W; Lull June M; Bannow Carol A; Lund Eric T; Mathews W Rodney
PY 2004
SO American journal of physiology. Endocrinology and metabolism, (2004 Feb) Vol. 286, No. 2, pp. E252-60. Electronic Publication: 2003-10-21. Journal code: 100901226. ISSN: 0193-1849.

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a-4.rag.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-728-679a-4.rag.

start

Go Back to previous page

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: June 12, 2006, 19:43:46 ; Search time 197 Seconds
(without alignments)
246.015 Million cell updates/sec

Title: US-10-728-679A-4
Perfect score: 573
Sequence: 1 MSMTSSVRVEWIAAVTIAAG.....KHNEETGDNVGPLIIKKKDT 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	573	100.0	106	8	ADP69732	Adp69732 Bovine mi
2	573	100.0	106	8	ADP75153	Adp75153 Bovine mi
3	534	93.2	108	2	AAW64556	Aaw64556 Human ost
4	534	93.2	108	2	AAY36115	Aay36115 Extended
5	534	93.2	108	7	ADF76839	Adf76839 Novel hum
6	534	93.2	108	7	ADJ69152	Adj69152 Human hea
7	534	93.2	108	7	ADJ69151	Adj69151 Human hea
8	534	93.2	108	8	ADP19423	Adp19423 Human sec
9	534	93.2	108	8	ADP69731	Adp69731 Human mit
10	534	93.2	108	8	ADP75154	Adp75154 Human mit
11	534	93.2	108	8	ABM81139	Abm81139 Tumour-as
12	534	93.2	108	9	ADY17444	Ady17444 PRO polyp
13	534	93.2	108	9	ADY20054	Ady20054 PRO polyp
14	487	85.0	108	8	ADP69733	Adp69733 Mouse mit
15	487	85.0	108	8	ADP75155	Adp75155 Murine mi
16	476	83.1	108	8	ADN99966	Adn99966 Novel hum
17	476	83.1	278	7	ADE08695	Ade08695 Novel pro
18	474.5	82.8	129	6	ABU89800	Abu89800 Novel hum
19	467	81.5	395	4	ABG17140	Abg17140 Novel hum
20	467	81.5	395	7	ADE10021	Ade10021 Novel pro
21	465.5	81.2	129	8	ADO09348	Ado09348 Novel hum
22	444	77.5	96	2	AAY12490	Aay12490 Human 5'
23	443	77.3	105	4	ABG17141	Abg17141 Novel hum
24	357	62.3	68	8	ABO57157	Abo57157 Human gen
25	350.5	61.2	131	8	ADN99967	Adn99967 Novel hum
26	350.5	61.2	131	8	ADP30143	Adp30143 Human sec
27	350.5	61.2	213	8	ADP29516	Adp29516 Human sec
28	350.5	61.2	232	8	ADP29515	Adp29515 Human sec
29	293.5	51.2	249	8	ADP29345	Adp29345 Human sec
30	292.5	51.0	119	4	ABB12110	Abb12110 Human tra
31	292.5	51.0	135	2	AAY32923	Aay32923 Transmemb
32	261.5	45.6	133	4	ABB58134	Abb58134 Drosophil
33	249	43.5	605	8	ADN22924	Adn22924 Bacterial
34	248.5	43.4	124	3	AAG01334	Aag01334 Human sec
35	211.5	36.9	119	5	ABB89268	Abb89268 Human pol
36	208.5	36.4	108	3	AAG54759	Aag54759 Arabidops
37	208.5	36.4	108	3	AAG46713	Aag46713 Arabidops
38	208.5	36.4	108	8	ADN74139	Adn74139 Thale cre
39	199.5	34.8	74	3	AAG46714	Aag46714 Arabidops
40	199.5	34.8	74	3	AAG54930	Aag54930 Arabidops
41	193.5	33.8	108	3	AAG20476	Aag20476 Arabidops
42	184.5	32.2	74	3	AAG20477	Aag20477 Arabidops
43	178.5	31.2	101	3	AAG05335	Aag05335 Arabidops
44	91.5	16.0	21	8	ADP75158	Adp75158 Murine mi
45	88.5	15.4	19	8	ADP75157	Adp75157 Murine mi
46	88.5	15.4	98	9	AEB40776	Aeb40776 L. pneumo
47	88.5	15.4	108	9	AEB37462	Aeb37462 L. pneumo
48	75	13.1	225	8	ADN47543	Adn47543 Thermococ
49	75	13.1	455	2	AAY28844	Aay28844 Aspergill
50	75	13.1	456	2	AAY28845	Aay28845 Redesigne
51	74.5	13.0	308	8	ADN21431	Adn21431 Bacterial
52	73.5	12.8	640	5	ABB53563	Abb53563 Lactococc
53	72.5	12.7	488	8	ADI67180	Adi67180 Lactobaci
54	72.5	12.7	627	5	ABP61041	Abp61041 Lactobaci
55	72.5	12.7	627	7	ADE12757	Ade12757 L. rhamno
56	71.5	12.5	359	8	ADS23577	Ads23577 Bacterial
57	71.5	12.5	456	8	ADR86000	Adr86000 Aspergill

SCORE Search Results Details f r Application 10728679 and Search Result us-10-728-679a-4.rai.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-72 679a-4.rai.

start

Go Back to previous pa

OM protein - protein search, using sw model

Run on: June 12, 2006, 19:52:31 ; Search time 50 Seconds
(without alignments)
185.565 Million cell updates/sec

Title: US-10-728-679A-4
Perfect score: 573
Sequence: 1 MSMTSSVRVEWIAAVTIAAG.....KHNEETGDNVGPLIIKKKDT 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : Issued_Patents_AA:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	444	77.5	96	2	US-09-621-976-7530	Sequence 7530, Ap
2	444	77.5	96	2	US-09-621-976-7532	Sequence 7532, Ap
3	295	51.5	71	2	US-09-621-976-7534	Sequence 7534, Ap
4	292.5	51.0	135	2	US-09-621-976-6779	Sequence 6779, Ap
5	248.5	43.4	124	2	US-09-513-999C-5415	Sequence 5415, Ap
6	212	37.0	50	2	US-09-621-976-7533	Sequence 7533, Ap
7	212	37.0	50	2	US-09-621-976-7535	Sequence 7535, Ap
8	206	36.0	50	2	US-09-621-976-7531	Sequence 7531, Ap
9	75	13.1	455	2	US-09-280-428A-6	Sequence 6, Appli
10	72.5	12.7	461	2	US-09-346-408-8	Sequence 8, Appli
11	72.5	12.7	488	2	US-09-634-238-272	Sequence 272, App
12	72.5	12.7	627	2	US-09-724-623-88	Sequence 88, Appl
13	72.5	12.7	627	3	US-10-288-930-88	Sequence 88, Appl
14	71	12.4	137	2	US-09-248-796A-26110	Sequence 26110, A
15	68.5	12.0	476	2	US-09-346-408-12	Sequence 12, Appl
16	67.5	11.8	300	2	US-09-902-540-14290	Sequence 14290, A
17	67	11.7	139	2	US-09-252-991A-18237	Sequence 18237, A
18	66	11.5	3542	2	US-10-087-013-2	Sequence 2, Appli
19	65	11.3	176	2	US-09-248-796A-20869	Sequence 20869, A
20	65	11.3	323	2	US-09-120-051D-31	Sequence 31, Appl
21	64.5	11.3	743	2	US-09-902-540-10164	Sequence 10164, A
22	64.5	11.3	866	2	US-09-902-540-10786	Sequence 10786, A
23	64	11.2	337	2	US-09-252-991A-27845	Sequence 27845, A
24	61.5	10.7	132	2	US-09-377-502-52	Sequence 52, Appl
25	61.5	10.7	214	2	US-09-328-352-6695	Sequence 6695, Ap
26	61.5	10.7	439	2	US-09-328-352-4576	Sequence 4576, Ap
27	61	10.6	425	2	US-08-946-329A-19	Sequence 19, Appl
28	61	10.6	425	2	US-08-567-357A-19	Sequence 19, Appl
29	61	10.6	425	2	US-08-729-743A-19	Sequence 19, Appl
30	61	10.6	425	2	US-08-349-498-19	Sequence 19, Appl
31	61	10.6	425	2	US-09-562-914-19	Sequence 19, Appl
32	61	10.6	425	5	PCT-US95-15463-19	Sequence 19, Appl
33	61	10.6	425	5	PCT-US95-15923-19	Sequence 19, Appl
34	61	10.6	463	2	US-09-902-540-13796	Sequence 13796, A
35	61	10.6	3080	7	5223423-4	Patent No. 5223423
36	60.5	10.6	139	2	US-09-543-681A-4567	Sequence 4567, Ap
37	60.5	10.6	380	2	US-09-248-796A-20364	Sequence 20364, A
38	60.5	10.6	501	2	US-09-367-206-3	Sequence 3, Appli
39	60.5	10.6	501	2	US-09-298-404-3	Sequence 3, Appli
40	60.5	10.6	845	2	US-09-949-016-8331	Sequence 8331, Ap
41	60.5	10.6	1503	2	US-08-976-255-14	Sequence 14, Appl
42	60.5	10.6	1703	2	US-09-824-574-3	Sequence 3, Appli
43	60.5	10.6	1703	2	US-09-487-558B-340	Sequence 340, App
44	60	10.5	487	2	US-09-627-650B-13	Sequence 13, Appl
45	60	10.5	487	2	US-09-436-063C-13	Sequence 13, Appl
46	60	10.5	488	2	US-09-543-681A-8263	Sequence 8263, Ap
47	59.5	10.4	169	2	US-09-270-767-33481	Sequence 33481, A
48	59.5	10.4	455	2	US-08-889-841B-46	Sequence 46, Appl
49	59.5	10.4	455	2	US-09-419-362-46	Sequence 46, Appl
50	59.5	10.4	749	2	US-09-562-737-93	Sequence 93, Appl
51	59.5	10.4	850	1	US-08-448-603A-28	Sequence 28, Appl
52	59.5	10.4	850	2	US-09-134-075-28	Sequence 28, Appl
53	59.5	10.4	850	2	US-09-492-739-28	Sequence 28, Appl
54	59.5	10.4	850	2	US-09-966-931A-28	Sequence 28, Appl
55	59	10.3	180	2	US-09-312-283C-375	Sequence 375, App
56	59	10.3	206	2	US-09-198-452A-824	Sequence 824, App
57	59	10.3	209	2	US-09-438-185A-777	Sequence 777, App
58	59	10.3	300	2	US-09-338-907-135	Sequence 135, App
59	59	10.3	300	2	US-09-218-207-135	Sequence 135, App
60	59	10.3	712	2	US-09-575-081B-10	Sequence 10, Appl

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-72
start

A;Cross-references: UNIPROT:O86333; UNIPARC:UPI00000D103F; GB:Z82098; GB:AL123456; NID
AAVVVVVTLAAIGYLIFEPKISGSSTSRQAASPTTPSPPSQVVVPIDLWNPDGVTVDLAD 116 Qy 66 KAVYCRC
V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Ke
NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: E84249 A;S
YKRFYVKDHRNKSMINPHIQ---------- 48 ||: ||: || | ||| : ||:||| : ||| | Db 133 VEYKHGVTLPSFAGLTAR
to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid B0432
Caenorhabditis elegans hypothetical protein B0432.3 Query Match 11.0%; Score 63; DB 2; Length
C0370w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15
C;Genetics: A;Map position: 3 A;Note: C0370w Query Match 11.0%; Score 63; DB 2; Length 430;
2S-3O] protein MJ0765 [similarity] - Methanococcus jannaschii N;Alternate names: prismane [6Fe-
A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; K
not shown; translation not shown A;Molecule type: DNA A;Residues: 1-548 A;Cross-references: UN
(covalent) #status predicted F;244,268,312,403,431,456,491/Binding site: 4Fe-2S-3O cluster (His
TNEVGYPGLKRIPVKEDGTKDFSEVIEHAKKCKPPTPLENGKIVGGFAHNQVLALADKVI 386 Qy 69 YC-RCWR
J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.
UNIPARC:UPI000005799B; GB:AE002326; GB:AE002160; NID:g7190614; PIDN:AAF39411.1; PID:
ARENIITSLEALGLFVRKEAYSSRVGVSYRSGAIIEPYLSKQWFVSVDSFRESLREFVNS 380 Qy 53 KVVHAFD
J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.;
A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: A82073 A;Status: p
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thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revis
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Y.; Kikuchi, H. DNA Res. 6, 83-101, 1999 A;Title: Complete genome sequence of an aerobic hyper-
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2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: C84970 R;Shigen
C;Genetics: A;Gene: flgK; BU346 Query Match 10.9%; Score 62.5; DB 2; Length 543; Best Local S

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 12, 2006, 19:47:36 ; Search time 39 Seconds
(without alignments)
261.512 Million cell updates/sec

Title: US-10-728-679A-4
Perfect score: 573
Sequence: 1 MSMTSSVRVEWIAAVTIAAG.....KHNEETGDNVGPLIIKKKDT 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	249	43.5	605	2	T26088	hypothetical prote
2	73.5	12.8	640	1	A86657	fructose-bisphosph
3	73	12.7	184	2	AC0769	probable acetyltra
4	72	12.6	1157	2	S38160	NUP133 protein - y
5	71.5	12.5	311	1	S48560	purine-nucleoside
6	69.5	12.1	873	2	B86471	hypothetical prote
7	69.5	12.1	915	2	C71455	alanine-tRNA ligas
8	69	12.0	923	2	G83826	hypothetical prote
9	68.5	12.0	338	2	B96976	probable ABC trans
10	68.5	12.0	476	2	S44943	sulfate adenylyltr
11	68.5	12.0	483	2	T14475	sulfate adenylyltr
12	68.5	12.0	914	2	B75017	alanyl-tRNA synthe
13	67	11.7	239	2	A69124	hypothetical prote
14	67	11.7	2510	2	T28160	hypothetical prote
15	66.5	11.6	432	2	T08944	hypothetical prote
16	66.5	11.6	730	2	G86161	hypothetical prote
17	65.5	11.4	194	2	G96924	sortase (surface p
18	64.5	11.3	384	2	AG2006	hypothetical prote
19	64	11.2	306	2	S47906	FAD synthetase - y
20	64	11.2	321	2	H83605	hypothetical prote
21	63.5	11.1	343	2	E70674	hypothetical prote
22	63.5	11.1	383	2	E84249	3-ketoacyl-CoA thi
23	63	11.0	180	2	T25460	hypothetical prote
24	63	11.0	430	2	T18433	hypothetical prote
25	63	11.0	548	2	E64395	hybrid cluster [4F
26	63	11.0	939	2	H81686	valyl-tRNA synthet
27	62.5	10.9	325	2	A82073	GTP-binding protei
28	62.5	10.9	359	2	E84674	hypothetical prote
29	62.5	10.9	403	2	C72546	probable coenzyme
30	62.5	10.9	543	2	C84970	flagellar hook-ass
31	62	10.8	142	2	JQ2280	low-temperature re
32	62	10.8	148	2	T23839	hypothetical prote
33	62	10.8	502	2	T23412	hypothetical prote
34	62	10.8	4196	2	T43274	dynein heavy chain
35	61	10.6	59	2	C72534	hypothetical prote
36	61	10.6	145	2	T15058	photosystem I prot
37	61	10.6	459	2	T51558	probable flavonol
38	61	10.6	461	2	T01825	hypothetical prote

39	61	10.6	550	2	H81718	methionyl-tRNA syn
40	61	10.6	658	2	A49362	carnitine O-palmit
41	61	10.6	917	2	T50979	related to tol pro
42	60.5	10.6	162	2	G90054	conserved hypothet
43	60.5	10.6	209	2	T39652	probable DNA J dom
44	60.5	10.6	604	2	AF0187	probable sideropho
45	60.5	10.6	619	2	S44669	ZK370.8 protein -
46	60.5	10.6	619	2	G84489	probable TNP2-like
47	60.5	10.6	943	2	C82559	isoleucyl-tRNA syn
48	60.5	10.6	1703	2	S15047	SNF2 protein - yea
49	60	10.5	182	2	C90986	probable transfera
50	60	10.5	182	2	F85831	probable transfera
51	60	10.5	182	2	E64971	hypothetical prote
52	60	10.5	355	2	C81405	probable oxidoredu
53	60	10.5	790	2	G59097	hypothetical prote
54	60	10.5	1106	2	T25065	hypothetical prote
55	60	10.5	1522	2	T39371	transcription regu
56	59.5	10.4	1206	2	E96507	hypothetical prote
57	59.5	10.4	1305	2	AB0168	probable cell divi
58	59	10.3	206	2	E86587	hypothetical prote
59	59	10.3	206	2	B72036	yggv family hypoth
60	59	10.3	319	2	PC1137	DNA primase - Buch

ALIGNMENTS

```
RESULT 1
T26088
hypothetical protein W02B12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26088
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z20149
A;Accession: T26088
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-605
A;Cross-references: UNIPROT:Q23124; UNIPARC:UPI00000802B8; EMBL:Z66521; PIDN:CAA91398.
A;Experimental source: clone W02B12
C;Genetics:
A;Gene: CESP:W02B12.7
A;Map position: 2
A;Introns: 30/1; 59/3; 134/2; 309/3; 424/3; 588/3

  Query Match             43.5%;  Score 249;  DB 2;  Length 605;
  Best Local Similarity   52.3%;  Pred. No. 5.4e-19;
  Matches   46;  Conservative   15;  Mismatches   23;  Indels    4;  Gaps    1;

Qy         17 IAAGTAAIGYLAYKRFYVKDHRNKSMINPHIQKDNPKVVHAFDMEDLGDKAVYCRCWRSK 76
              : || | ||||   :|  :  |     |  || |: |:|   |:|||:|:|  :|||||:|:
Db         49 VLAGGALIGYLVGYKFGQRSAR----CNYKIQLDSNKIVDTVDIEDIGEKKAFCRCWKSE 104

Qy         77 KFPLCDGSHTKHNEETGDNVGPLIIKKK 104
              |:| ||||| |||:||||||||||:| :
Db        105 KWPYCDGSHGKHNKETGDNVGPLIVKSE 132


RESULT 2
```

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a-4.rup.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-728-679a-4.rup.

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OM protein - protein search, using sw model

Run on: June 12, 2006, 19:44:06 ; Search time 294 Seconds
(without alignments)
333.509 Million cell updates/sec

Title: US-10-728-679A-4
Perfect score: 573
Sequence: 1 MSMTSSVRVEWIAAVTIAAG.....KHNEETGDNVGPLIIKKKDT 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	572	99.8	106	2	Q3ZBU2_BOVIN	Q3zbu2 bos taurus
2	534	93.2	108	1	CJ070_HUMAN	Q9nz45 homo sapien
3	487	85.0	108	1	CJ070_MOUSE	Q91ws0 mus musculu
4	487	85.0	108	2	Q3V2I3_MOUSE	Q3v2i3 m 10 day ol

5	413.5	72.2	103	2	Q6GLC0_XENTR	Q6glc0 xenopus tro
6	399.5	69.7	103	2	Q66J28_XENLA	Q66j28 xenopus lae
7	393.5	68.7	103	2	Q52L36_XENLA	Q52l36 xenopus lae
8	372.5	65.0	107	2	Q6PGY7_BRARE	Q6pgy7 brachydanio
9	317	55.3	121	2	Q58EB0_BRARE	Q58eb0 brachydanio
10	295.5	51.6	135	2	Q9D0Y0_MOUSE	Q9d0y0 mus musculu
11	295.5	51.6	135	2	Q6PCF8_XENLA	Q6pcf8 xenopus lae
12	293.5	51.2	135	2	Q9CQB5_MOUSE	Q9cqb5 m adult mal
13	293	51.1	135	2	Q6AZG1_XENLA	Q6azg1 xenopus lae
14	292.5	51.0	135	2	Q8N5K1_HUMAN	Q8n5k1 homo sapien
15	292.5	51.0	135	2	Q5I027_XENTR	Q5i027 xenopus tro
16	292.5	51.0	150	2	Q7Z3D5_HUMAN	Q7z3d5 homo sapien
17	278.5	48.6	99	2	Q4PM74_IXOSC	Q4pm74 ixodes scap
18	277	48.3	134	2	Q4SDL1_TETNG	Q4sdl1 tetraodon n
19	274	47.8	135	2	Q7T326_BRARE	Q7t326 brachydanio
20	273.5	47.7	99	2	Q6B8D1_9ACAR	Q6b8d1 ixodes paci
21	261.5	45.6	133	2	Q9VAM6_DROME	Q9vam6 drosophila
22	249	43.5	103	2	Q5FC71_CAEEL	Q5fc71 caenorhabdi
23	249	43.5	605	2	Q9NL51_CAEEL	Q9nl51 caenorhabdi
24	245	42.8	132	2	Q86FB3_SCHJA	Q86fb3 schistosoma
25	217.5	38.0	129	2	Q7QA13_ANOGA	Q7qa13 anopheles g
26	208.5	36.4	108	2	Q9FLI7_ARATH	Q9fli7 arabidopsis
27	193.5	33.8	108	2	Q8LCD5_ARATH	Q8lcd5 arabidopsis
28	175.5	30.6	91	2	Q4T7B9_TETNG	Q4t7b9 tetraodon n
29	132.5	23.1	141	2	Q4N2P5_THEPA	Q4n2p5 theileria p
30	122.5	21.4	145	2	Q55GD7_DICDI	Q55gd7 dictyosteli
31	112.5	19.6	152	2	Q9NDU7_PLAF7	Q9ndu7 plasmodium
32	111.5	19.5	176	2	Q4Z5J0_PLABE	Q4z5j0 plasmodium
33	111	19.4	130	2	Q4XH00_PLACH	Q4xh00 plasmodium
34	109	19.0	152	2	Q962M3_PLAVI	Q962m3 plasmodium
35	103	18.0	94	2	Q7RKN6_PLAYO	Q7rkn6 plasmodium
36	102	17.8	79	2	Q4Z0D3_PLABE	Q4z0d3 plasmodium
37	92.5	16.1	102	2	Q4N226_THEPA	Q4n226 theileria p
38	91.5	16.0	210	2	Q3C6G4_9CLOT	Q3c6g4 alkaliphilu
39	90.5	15.8	90	2	Q5WYF7_LEGPL	Q5wyf7 legionella
40	90	15.7	208	2	Q98DK7_RHILO	Q98dk7 rhizobium l
41	89.5	15.6	120	2	Q4FWY2_LEIMA	Q4fwy2 leishmania
42	89	15.5	310	2	Q54UZ7_DICDI	Q54uz7 dictyosteli
43	88.5	15.4	98	2	Q5X705_LEGPA	Q5x705 legionella
44	88.5	15.4	98	2	Q5ZXI8_LEGPH	Q5zxi8 legionella
45	88	15.4	211	2	Q41MS8_METBU	Q41ms8 methanococc
46	86	15.0	229	2	Q429J3_DESHA	Q429j3 desulfitoba
47	85	14.8	513	2	Q87I40_VIBPA	Q87i40 vibrio para
48	83.5	14.6	78	2	Q4FPC6_PELUB	Q4fpc6 pelagibacte
49	83	14.5	512	2	Q4FPC4_PELUB	Q4fpc4 pelagibacte
50	82	14.3	93	2	Q31MJ2_SYNP7	Q31mj2 synechococc
51	82	14.3	93	2	Q5MZD7_SYNP6	Q5mzd7 synechococc
52	81.5	14.2	397	2	O76947_HYDMA	O76947 hydra magni
53	78	13.6	516	2	Q33UW6_9GAMM	Q33uw6 shewanella
54	76.5	13.4	96	2	Q30RV3_THIDN	Q30rv3 thiomicrosp
55	76.5	13.4	256	2	Q465J8_METBA	Q465j8 methanosarc
56	76	13.3	55	2	Q2S5U2_9SPHI	Q2s5u2 salinibacte
57	76	13.3	69	2	Q9HLZ0_THEAC	Q9hlz0 thermoplasm
58	76	13.3	94	2	Q3XVQ6_9PROT	Q3xvq6 magnetococc
59	75.5	13.2	1308	2	Q8IK00_PLAF7	Q8ik00 plasmodium
60	75	13.1	225	1	PYRH_PYRKO	Q5jfz7 pyrococcus

ALIGNMENTS

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a-4.p2n.rge.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-728-679a-4.p2n.rge.

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```
                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:          June 14, 2006, 06:36:26 ; Search time 2875 Seconds
                                           (without alignments)
                                           3536.570 Million cell updates/sec

Title:           US-10-728-679A-4
Perfect score:   573
Sequence:        1 MSMTSSVRVEWIAAVTIAAG.........KHNEETGDNVGPLIIKKKDT 106

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10728679/runat_12062006_151405_7711/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=60
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10728679_@CGN_1_1_8328_@runat_12062006_151405_7711 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       GenEmbl:*
                 1:  gb_env:*
```

2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	572	99.8	767	14	BC103105	BC103105 Bos tauru
2	534	93.2	324	2	BD063608	BD063608 Human pro
3	534	93.2	470	2	CQ699231	CQ699231 Sequence
4	534	93.2	599	2	CQ701260	CQ701260 Sequence
5	534	93.2	631	2	BD139505	BD139505 Extended
6	534	93.2	636	2	CS033743	CS033743 Sequence
7	534	93.2	636	2	CS036353	CS036353 Sequence
8	534	93.2	636	2	CS042695	CS042695 Sequence
9	534	93.2	636	2	CS045305	CS045305 Sequence
10	534	93.2	636	5	AF220049	AF220049 Homo sapi
11	534	93.2	638	5	BC007043	BC007043 Homo sapi
12	534	93.2	672	5	BC008474	BC008474 Homo sapi
13	534	93.2	683	5	BC005962	BC005962 Homo sapi
14	534	93.2	893	2	BD063633	BD063633 Human pro
15	534	93.2	925	5	BC059168	BC059168 Homo sapi
16	507	88.5	597	2	AX972869	AX972869 Sequence
17	507	88.5	597	2	BD111588	BD111588 EST and e
18	507	88.5	597	2	AR416035	AR416035 Sequence
19	487	85.0	740	6	BC013522	BC013522 Mus muscu
20	487	85.0	773	6	BC019860	BC019860 Mus muscu
21	487	85.0	792	6	BC021952	BC021952 Mus muscu
22	485	84.6	550	2	AX972867	AX972867 Sequence
23	485	84.6	550	2	BD111586	BD111586 EST and e
24	485	84.6	550	2	AR416033	AR416033 Sequence
25	481.5	84.0	504	2	AX972870	AX972870 Sequence
26	481.5	84.0	504	2	AX972872	AX972872 Sequence
27	481.5	84.0	504	2	BD111589	BD111589 EST and e
28	481.5	84.0	504	2	BD111591	BD111591 EST and e
29	481.5	84.0	504	2	AR416036	AR416036 Sequence
30	481.5	84.0	504	2	AR416038	AR416038 Sequence
31	476	83.1	129542	5	AC013400	AC013400 Homo sapi
32	475.5	83.0	514	2	AX972868	AX972868 Sequence
33	475.5	83.0	514	2	BD111587	BD111587 EST and e
34	475.5	83.0	514	2	AR416034	AR416034 Sequence
35	467	81.5	396	2	CQ732663	CQ732663 Sequence
c 36	467	81.5	158395	5	AC079600	AC079600 Homo sapi
37	466	81.3	426	2	AX972871	AX972871 Sequence

	38	466	81.3	426	2	BD111590	BD111590 EST and e
	39	466	81.3	426	2	AR416037	AR416037 Sequence
	40	444	77.5	398	2	BD076313	BD076313 5' EST of
	41	441.5	77.1	127259	5	AC008562	AC008562 Homo sapi
	42	441.5	77.1	133658	5	AC008489	AC008489 Homo sapi
c	43	432	75.4	618	2	AX277139	AX277139 Sequence
	44	414.5	72.3	1016	11	CT027940	CT027940 Xenopus t
	45	414.5	72.3	1674	11	BC074579	BC074579 Xenopus t
c	46	408	71.2	200966	6	AL596108	AL596108 Mouse DNA
c	47	407	71.0	653	2	AX421535	AX421535 Sequence
	48	404	70.5	72234	12	AC016467	AC016467 Homo sapi
	49	400.5	69.9	865	11	BC081083	BC081083 Xenopus l
	50	394.5	68.8	1447	11	BC094083	BC094083 Xenopus l
	51	382	66.7	218075	12	AC161920	AC161920 Bos tauru
	52	372.5	65.0	1985	11	BC056783	BC056783 Danio rer
	53	368.5	64.3	334	2	CQ729743	CQ729743 Sequence
	54	361	63.0	151766	5	AC016396	AC016396 Homo sapi
	55	361	63.0	182433	12	AL358155	AL358155 Homo sapi
c	56	349.5	61.0	202518	12	AC151932	AC151932 Otolemur
c	57	349.5	61.0	241656	12	AC146647	AC146647 Otolemur
	58	337	58.8	645	2	CQ736520	CQ736520 Sequence
	59	323	56.4	163328	6	AC156270	AC156270 Mus muscu
c	60	321	56.0	83864	12	AC135538	AC135538 Rattus no

ALIGNMENTS

RESULT 1
BC103105

LOCUS BC103105 767 bp mRNA linear MAM 07-FEB-2006

DEFINITION Bos taurus similar to Uncharacterized hematopoietic stem/progenitor cells protein MDS029, mRNA (cDNA clone MGC:128185 IMAGE:7985894), complete cds.

ACCESSION BC103105

VERSION BC103105.1 GI:73587066

KEYWORDS MGC.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 767)

AUTHORS Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y., Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber,K., Shenmen,C., Wagner,L., Bala,M., Barbazuk,S., Barber,S., Babakaiff,R., Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R., Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J., Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2005) BC Cancer Agency, Canada's Michael Smith Genome Sciences Centre, Suite 100, 570 West 7th Avenue, Vancouver, British Columbia V5Z 4S6, Canada

REMARK NIH-MGC Project

COMMENT Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robertk@bcgsc.ca

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a-4.p2n.rng.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-728-679a-4.p2n.rng.

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```
                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:          June 14, 2006, 06:36:14 ; Search time 517 Seconds
                                           (without alignments)
                                           2144.270 Million cell updates/sec

Title:           US-10-728-679A-4
Perfect score:   573
Sequence:        1 MSMTSSVRVEWIAAVTIAAG.........KHNEETGDNVGPLIIKKKDT 106

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10728679/runat_12062006_151400_7661/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=60
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10728679_@CGN_1_1_761_@runat_12062006_151400_7661 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_8:*
                 1:  geneseqn1980s:*
```

2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	572	99.8	655	12	ADP75150	Adp75150 Bovine mi
	2	534	93.2	324	2	AAV49595	Aav49595 Human Ost
	3	534	93.2	487	9	ACH41927	Ach41927 Human foe
	4	534	93.2	491	9	ACH22155	Ach22155 Human adu
	5	534	93.2	602	6	ABK34426	Abk34426 Human cDN
	6	534	93.2	631	2	AAX97799	Aax97799 Extended
	7	534	93.2	631	12	ADP19066	Adp19066 Human sec
	8	534	93.2	636	10	ADF76838	Adf76838 Novel hum
	9	534	93.2	636	12	ADP69730	Adp69730 Human mit
	10	534	93.2	636	12	ADP75151	Adp75151 Human mit
	11	534	93.2	636	13	ACN39056	Acn39056 Tumour-as
	12	534	93.2	636	14	ADY20053	Ady20053 DNA encod
	13	534	93.2	636	14	ADY17443	Ady17443 DNA encod
	14	534	93.2	893	2	AAV49594	Aav49594 Human Ost
	15	487	85.0	792	12	ADP75152	Adp75152 Murine mi
	16	476	83.1	327	12	ADO00751	Ado00751 Novel hum
	17	476	83.1	327	12	ADN99182	Adn99182 Novel hum
	18	476	83.1	837	10	ADE07784	Ade07784 Novel cod
	19	474.5	82.8	400	8	ACA90177	Aca90177 cDNA enco
	20	471	82.2	507	2	AAX90806	Aax90806 Rat progr
	21	467	81.5	396	12	ADO00752	Ado00752 Novel hum
	22	467	81.5	396	12	ADN99183	Adn99183 Novel hum
	23	467	81.5	396	12	ADP28912	Adp28912 Human sec
	24	467	81.5	642	12	ADP28285	Adp28285 Human sec
	25	467	81.5	699	12	ADP28284	Adp28284 Human sec
	26	467	81.5	1188	5	AAS81327	Aas81327 DNA encod
	27	467	81.5	1188	10	ADE09887	Ade09887 Novel DNA
	28	458	79.9	851	5	AAS81328	Aas81328 DNA encod
	29	444	77.5	398	2	AAX41323	Aax41323 Human sec
c	30	444	77.5	435	7	ADS71913	Ads71913 Human kid
c	31	444	77.5	435	7	ADS72740	Ads72740 Human kid
c	32	444	77.5	435	7	ADS72079	Ads72079 Human kid
c	33	444	77.5	435	7	ADW40933	Adw40933 cDNA elev
c	34	444	77.5	435	7	ADW41594	Adw41594 cDNA elev
c	35	444	77.5	435	7	ADW40767	Adw40767 cDNA elev
	36	442.5	77.2	396	12	ADO09347	Ado09347 Novel hum
c	37	432	75.4	618	4	AAS32966	Aas32966 DNA encod

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a 4.p2n.rni.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-72 4.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on:         June 14, 2006, 06:53:14 ; Search time 169 Seconds
                                          (without alignments)
                                          1760.392 Million cell updates/sec

Title:          US-10-728-679A-4
Perfect score:  573
Sequence:       1 MSMTSSVRVEWIAAVTIAAG.........KHNEETGDNVGPLIIKKKDT 106

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10728679/runat_12062006_151413_7816/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=60 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss08 -USER=US10728679_@CGN_1_1_204_@runat_12062006_151413_7816 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Issued_Patents_NA:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
```

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		507	88.5	597	3	US-09-621-976-3672	Sequence 3672, Ap
2		485	84.6	550	3	US-09-621-976-3670	Sequence 3670, Ap
3		481.5	84.0	504	3	US-09-621-976-3673	Sequence 3673, Ap
4		481.5	84.0	504	3	US-09-621-976-3675	Sequence 3675, Ap
5		475.5	83.0	514	3	US-09-621-976-3671	Sequence 3671, Ap
6		466	81.3	426	3	US-09-621-976-3674	Sequence 3674, Ap
7		292.5	51.0	575	3	US-09-621-976-2919	Sequence 2919, Ap
8		248.5	43.4	418	3	US-09-513-999C-1338	Sequence 1338, Ap
9		76	13.3	601	3	US-09-949-016-19826	Sequence 19826, A
10		76	13.3	601	3	US-09-949-016-157705	Sequence 157705,
11		75	13.1	1371	3	US-09-280-428A-12	Sequence 12, Appl
12		75	13.1	1589	3	US-09-280-428A-5	Sequence 5, Appli
13	c	75	13.1	2281	3	US-09-949-016-104	Sequence 104, App
14	c	75	13.1	2281	3	US-09-949-016-4398	Sequence 4398, Ap
15	c	75	13.1	6870	5	US-09-543-679A-2522	Sequence 2522, Ap
16	c	75	13.1	8055	5	US-09-543-679A-2523	Sequence 2523, Ap
17	c	75	13.1	10029	3	US-09-949-016-11846	Sequence 11846, A
18	c	75	13.1	10029	3	US-09-949-016-16140	Sequence 16140, A
19	c	75	13.1	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
20	c	72.5	12.7	947	3	US-09-270-767-1368	Sequence 1368, Ap
21	c	72.5	12.7	947	3	US-09-270-767-16650	Sequence 16650, A
22		72.5	12.7	1881	3	US-09-724-623-26	Sequence 26, Appl
23		72.5	12.7	1881	5	US-10-288-930-26	Sequence 26, Appl
24		72.5	12.7	1890	3	US-09-346-408-7	Sequence 7, Appli
25		72.5	12.7	2174	3	US-09-634-238-54	Sequence 54, Appl
26		72	12.6	222	5	US-09-974-300-4137	Sequence 4137, Ap
27		71.5	12.5	1486	3	US-09-533-559-5542	Sequence 5542, Ap
28		71	12.4	414	3	US-09-248-796A-12007	Sequence 12007, A
29	c	68.5	12.0	606	3	US-09-540-236-1193	Sequence 1193, Ap
30	c	68.5	12.0	22407	3	US-09-596-002-16	Sequence 16, Appl
31	c	68	11.9	5760	3	US-10-152-886-14	Sequence 14, Appl
32	c	67.5	11.8	782	3	US-09-270-767-15186	Sequence 15186, A
33		67.5	11.8	903	3	US-09-902-540-7076	Sequence 7076, Ap
34		67.5	11.8	3609	3	US-09-902-540-632	Sequence 632, App
35		67	11.7	420	3	US-09-252-991A-1666	Sequence 1666, Ap
36	c	67	11.7	700	3	US-09-735-271-93	Sequence 93, Appl
37	c	67	11.7	700	3	US-09-735-271-94	Sequence 94, Appl
38		67	11.7	4293	3	US-09-252-991A-1619	Sequence 1619, Ap
39	c	67	11.7	4359	3	US-09-252-991A-1547	Sequence 1547, Ap
40		67	11.7	11907	3	US-08-061-376-4	Sequence 4, Appli
41		66	11.5	879	3	US-09-328-352-697	Sequence 697, App
42		66	11.5	10628	3	US-10-087-013-1	Sequence 1, Appli
43	c	66	11.5	71574	3	US-09-949-016-15580	Sequence 15580, A

SCORE Search Results Details for Application 10728679 and Search Result us-10-728-679a-4.p2n.rst.

This page gives you Search Results detail for the Application 10728679 and Search Result us-10-728-679a-4.p2n.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on:         June 14, 2006, 06:44:01 ; Search time 4441 Seconds
                                           (without alignments)
                                           2002.066 Million cell updates/sec

Title:          US-10-728-679A-4
Perfect score:  573
Sequence:       1 MSMTSSVRVEWIAAVTIAAG.........KHNEETGDNVGPLIIKKKDT 106

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10728679/runat_12062006_151409_7769/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=60
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10728679_@CGN_1_1_9528_@runat_12062006_151409_7769 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                1:  gb_est1:*
```

2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	572	99.8	449	10	DY188817	DY188817 991215BAB
	2	572	99.8	515	2	BM432127	BM432127 1JEJ16G10
	3	572	99.8	559	1	AV606301	AV606301 AV606301
c	4	572	99.8	586	5	CK943800	CK943800 4067940 B
	5	572	99.8	598	10	DV844638	DV844638 LB01220.C
	6	572	99.8	606	10	DV842169	DV842169 LB01210.C
	7	572	99.8	606	10	DV845395	DV845395 LB01223.C
	8	572	99.8	614	10	DV920567	DV920567 LB02922.C
	9	572	99.8	615	7	BF231164	BF231164 253428 BA
	10	572	99.8	621	4	CB465697	CB465697 727760 MA
	11	572	99.8	642	10	DV825472	DV825472 LB02023.C
	12	572	99.8	642	10	DV837687	DV837687 LB01117.C
	13	572	99.8	654	10	DT720366	DT720366 LB0114.CR
c	14	572	99.8	655	4	CB464717	CB464717 725942 MA
	15	572	99.8	662	10	DT825854	DT825854 LB00240.C
	16	572	99.8	666	10	DV826326	DV826326 LB02027.C
	17	572	99.8	668	10	DV827858	DV827858 LB0191.CR
	18	572	99.8	679	10	DV847404	DV847404 LB0125.CR
	19	572	99.8	680	4	CB463270	CB463270 723638 MA
	20	572	99.8	681	10	DV803159	DV803159 LB01324.C
	21	572	99.8	696	8	CN789430	CN789430 4123892 B
	22	572	99.8	703	10	DV846432	DV846432 LB01227.C
	23	572	99.8	704	10	DV826561	DV826561 LB02029.C
	24	572	99.8	712	10	DV843777	DV843777 LB01216.C
	25	572	99.8	735	10	DV830111	DV830111 LB01913.C
	26	572	99.8	737	10	DV826919	DV826919 LB02031.C
	27	572	99.8	742	10	DV847709	DV847709 LB0126.CR
	28	572	99.8	756	10	DT854204	DT854204 LB00514.C
	29	572	99.8	756	10	DT857017	DT857017 LB00529.C
	30	572	99.8	768	10	DT720866	DT720866 LB0122.CR
	31	572	99.8	768	10	DV848439	DV848439 LB0129.CR
	32	572	99.8	780	10	DV841104	DV841104 LB0115.CR
	33	572	99.8	785	9	DN549625	DN549625 1407931 M
	34	572	99.8	789	10	DV824472	DV824472 LB02018.C
	35	572	99.8	832	10	DV848261	DV848261 LB0128.CR
	36	567	99.0	460	10	DY198338	DY198338 991215BAB
c	37	562	98.1	704	9	CX949065	CX949065 UMC-bcl_0
	38	561	97.9	536	7	BE668837	BE668837 159214 MA